

SEQUENCE LISTING

- (1) GENERAL INFORMATION
 - (i) APPLICANT: Hillman, Jennifer L.
Goli, Surya K.
 - (ii) TITLE OF THE INVENTION: NOVEL TUMORIGENESIS PROTEIN
 - (iii) NUMBER OF SEQUENCES: 3
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Genomics, Inc.
 - (B) STREET: 3160 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/183,825
 - (B) FILING DATE: October 30, 1998
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/822,260
 - (B) FILING DATE: March 20, 1997
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0247-2 CON
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166
 - (C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: UTRSNOT02
 - (B) CLONE: 2267574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Ser Glu Ser Val Gln Lys Gly Phe Gln Met Leu Ala Asp
 1 5 10 15
 Pro Arg Ser Phe Asp Ser Asn Ala Phe Thr Leu Leu Arg Ala Ala
 20 25 30
 Phe Gln Ser Leu Leu Asp Ala Gln Ala Asp Glu Ala Val Leu Asp His
 35 40 45
 Pro Asp Leu Lys His Ile Asp Pro Val Val Leu Lys His Cys His Ala
 50 55 60
 Ala Ala Ala Thr Tyr Ile Leu Glu Ala Gly Lys His Arg Ala Asp Lys
 65 70 75 80
 Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu Arg
 85 90 95
 Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu Glu
 100 105 110
 Ile Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp Val
 115 120 125
 Ser Trp Arg Leu Glu Tyr Gln Ile Lys Thr Asn Gln Leu His Arg Met
 130 135 140
 Tyr Arg Pro Ala Tyr Leu Val Thr Leu Ser Val Gln Asn Thr Asp Ser
 145 150 155 160
 Pro Ser Tyr Glu Ile Ser Phe Ser Cys Ser Met Glu Gln Leu Gln
 165 170 175
 Asp Leu Val Gly Lys Leu Lys Asp Ala Ser Lys Ser Leu Glu Arg Ala
 180 185 190
 Thr Gln Leu
 195

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSN02
 (B) CLONE: 2267574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGAAGTCACG GCGGCTCAC AATGGAGCTC TCGGAGTCTG TGCAGAAAGG CTTCAGATG 60
 CTGGCGGATC CCCGCTCCTT CGACTCCAAC GCCTTCACGC TTCTCCTCCG GCGGCGATTC 120
 CAGAGTCTGC TGGACGCCCA GGCGGACGAG GCCGTGTTAG ATCATCCAGA CTGAAACAT 180
 ATCGACCCAG TGGTTTAAAA ACATGTGTCAT GCAGCAGCTG CAACTTACAT ACTAGAGGCA 240
 GGAAAGCACC GAGCTGACAA GTCAACTCTA AGCACTTATC TAGAAGACTG TAAATTTGAC 300
 AGAGAGCGAA TAGAACTGTT TTGCACGGAA TATCAGAATA ATAAGAAATC CCTAGAAATC 360
 CTACTGGGAA GTATAGGCAG ATCTCTCCCT CATATAACGG ATGTTTCTTG GCGCTTGGAA 420
 TATCAGATAA AGACCAATCA ACTTCATAGG ATGTACAGAC CTGCATATTT GGTGACCTTA 480
 AGTGTACAGA ACACGTGATT CCATCTCTAT CCAGAGATTA GTTTTAGTTG CAGCATGGAA 540
 CAATTACAGG ACTTGGTGGG GAAACTTAA GATGCTTCGA AAAGCCTGGA AGAGCAACT 600
 CAGTTTAACT TTGGGGAAGT TAACGATCCG CCCGAGTGCA GAGGAAACC AGAAACGCTT 660
 TGCCTTCACG TGAAACCCCG TTTGTGCGAG CTGGATGTCC TTTTCAGTAG AAAAGAATT 720
 TCCTTTTGAA TTTATACCAT TCANCAATTT T 751

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 265569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Glu	Leu	Ser	Glu	Ser	Val	Gln	Arg	Gly	Ile	Gln	Thr	Leu	Ala	Asp
1				5					10					15	
Pro	Gly	Ser	Phe	Asp	Ser	Asn	Ala	Phe	Ala	Leu	Leu	Leu	Arg	Ala	Ala
			20				25						30		
Phe	Gln	Ser	Leu	Leu	Asp	Ala	Arg	Ala	Asp	Glu	Ala	Ala	Leu	Asp	His
			35				40					45			
Pro	Tyr	Leu	Lys	Gln	Ile	Asp	Pro	Val	Val	Leu	Lys	His	Cys	His	Ala
	50				55					60					
Ala	Ala	Ala	Thr	Cys	Ile	Leu	Glu	Ala	Gly	Lys	His	Gln	Val	Asp	Lys
65				70					75					80	
Ser	Thr	Leu	Ser	Thr	Tyr	Leu	Glu	Asp	Cys	Lys	Phe	Asp	Arg	Glu	Arg
			85						90					95	
Ile	Glu	Leu	Phe	Cys	Thr	Glu	Tyr	Gln	Asn	Asn	Lys	Asn	Ser	Leu	Glu
			100					105						110	
Thr	Leu	Leu	Gly	Ser	Ile	Gly	Arg	Ser	Leu	Pro	His	Ile	Thr	Asp	Val
			115					120							
Ser	Trp	Arg	Leu	Glu	Tyr	Gln	Ile	Lys	Thr	Asn	Gln	Leu	His	Lys	Met
	130					135				140					
Tyr	Arg	Pro	Gly	Tyr	Leu	Val	Thr	Leu	Asn	Val	Glu	Asn	Asn	Asp	Ser
145					150					155				160	
Gln	Ser	Tyr	Pro	Glu	Ile	Asn	Phe	Ser	Cys	Asn	Met	Glu	Gln	Leu	Gln
				165				170						175	
Asp	Leu	Val	Gly	Lys	Leu	Lys	Asp	Ala	Ser	Lys	Ser	Leu	Glu	Arg	Ala
			180				185							190	
Thr	Gln	Leu													
			195												